

1/3

*	20	*	40	*	60	*		
axmi007	-----VQNQ-NMVEIIFDSKNL SYPNSNRNIDHSRMPYIINNQPEPOMTAWEDQULNCQGNTQYGDNFETFAS						: 67	
crylAa	-----MDNP---NINECIPNCLSNMSEVEGLGG						: 26	
crylAc	-----MDNP---NINECIPNCLSNMSEVEGLGG						: 26	
crylIa	-----MKLKQDKHOSFSNAKVD--K1STD--LKDIELOMIDHEDCPKNSSEYEN						: 50	
cry3Aa1	MIRKGGRKPNPNSRSEDTIKYIENNE--YPTINHQQELAEITPTIILWEEFPERATADNN-----TE						: 63	
cry3Ba	MIRMGGRKXMPNSRSEDTIKVPMSE--LPTINHQQELADENSTEEELNMEFPERATADNS-----TE						: 63	
cry4Aa	-----HNPYQKNEVETINASOKKLN--ISNNTYTPEIEMS EKOLEQSTMDQULNCQDQOQ-----YGG						: 59	
cry6Aa							:	
cry7Aa	-----MILNMILDGYEDSNR--TLMNSLMETOKALSPS DMMMDLTS TEREQP-----						: 49	
cry8Aa	-----MSPNQMEVILIDATPSTS--YSSDSNRYPFAPEPTDALDMMDYMKQSGGEMPEL-----FG						: 58	
cry10Aa	-----MNPYQKNEVIFNAPSFGFS--KSNNYNSRYCLAKMKNOPRKTINMDQULNCQDQYCGNN-----AG						: 62	
cry16Aa	-----MHYGURNEEDLNPASSD--NMNSNTYPRYBLAQPOQDLMQDINMADQULNCCEGYHIENP-----RE						: 61	
cry19Ba	-----MNSYQKNEVILDAKRMTC--HMSNCYPKPLAIDQMYPRMTHADQHADCEASYAS-----						: 58	
cry24Aa	-----HNPYQKNEVILDESSQNMN--MPPNRYPQADDENAVQKQGMDQULNCCEGSN-----						: 52	
	n ey	n	YP	p	nykd			
	80	*	100	*	120	*	140	*
axmi007	ADTIAAVSAGTIYSGTIPAGIGELTSISGPIGIGAHLISFGTISYFQDAGEQDKTVTDFPDKGELFVYDTPT							: 142
crylAa	-----ERIETGYPTIDISLSITOFIISSEF--MDCAGFVLGLVDIIMUGIFCFSQ-----MDAPPVQDQDQIIMQIE							: 89
crylAc	-----ERIETGYPTIDISLSITOFIISSEF--MVEGAGFVLGLVDIIMUGIFCFSQ-----MDAPPVQDQDQIIMQIE							: 89
crylIa	-----VEPFVSASTIQTGCHQAKDQGTLG--VFAQGASLSPFEGELMS-KG--KNOEILPEHVEIENOKKS							: 117
cry3Aa1	ALDSSTIKDVKQKCSVWEDLHGVVG--FIFGGAAVSVFVNFNTIQS--EDPNAKAEQEVQABMDQKIA							: 130
cry3Ba	VLDSSITVKDAVGTGCSVQGQHGVVG--VFAQAGTSFQSFNALQSD--ADPNAKAEQEVQABMDQKIE							: 131
cry4Aa	-----DFETFDGSEIATVQGTVHGTGFG--FTTPLGLAIGCTGTLFPELEAQDSN-TUSDPEITQTKWIKKEDIA							: 130
cry6Aa								:
cry7Aa	-----EALASGNTAINTVSVIATPSALG--VEGASTHNTFLKAGELDENG--KI--DEPATEVEABMDQKIE							: 116
cry8Aa	NPETFISSSTIQTGCHQEVMDIGALG--VFAQASLSPFENGQDLSKS--VDINGEIVRVEFVYDQKIE							: 127
cry10Aa	NFASSETTIVGUSACHIVVGTMCAGAFA--AVVLAACIISGTMIPFNGSDPAN--VUQDPLMIGGRPIDEID							: 131
cry16Aa	ASVRAGLGKGELIVVSVIHEFFGFS--IILDITGLYQOISELLDEEDDTQYIQUDIDENHCDLIDKQIT							: 128
cry19Ba	-----GPSQLFKVGGSHWAKDQG--MIPEDGPLSWSWSPFQTEIEKNTVQEDMVKYVANHKGQIT							: 120
cry24Aa	-----ISPSPAATTSKISWISIMPTIAKAVASSLADSUKSSLGISKTLTENNVS--QVSIVVQVHOQMRDQ							: 117
	g lg	p	p	w f	e	q		
	160	*	180	*	200	*	220	*
axmi007	ESTIQLKQHOTIECFRQIHDQ-SNTAIDDDURKLRLQAPGLPPSSALQQAALTLKIRFENVHNDPTEIPGFQLE-							: 215
crylAa	-----EFAMQNSRIFGQISLQY-IAAESFREDEAPTN--PALREEMRQDNDINSALTTAELFAVQN-----							: 152
crylAc	-----EFAMQNSRIFGQISLQY-IAAESFREDEAPTN--PALREEMRQDNDINSALTTAELFAVQN-----							: 152
crylIa	TYAIIKKAIDTQKPCGDATA-VHDSPELSQUVGQNN--TRASVSKSQTIAELMEVQKESFAVSG							: 180
cry3Aa1	DYATIJKKAELDQGQDNE-DEVSAPSSTQKUPVSS--RNPHSQGRDPELSQAEHRSNMSFSAISG							: 196
cry3Ba	-----EYAISSKKAELDQGQDNE-DYVNAIDSTKKAPVNL--RSRRSQRDPELSQAEHRSNMSFAVSK							: 197
cry4Aa	STYISNENKIIERSFVWIS-TWNNHKTMEQPN--PQNTDQWRTQIQLWYHQNVDLVLNSCPN							: 195
cry6Aa								:
cry7Aa	-----EYVVKKAELDQGQDNE-KKQKAQADLKGODD--PEAIALSQTAEFRIIDSLPEFSWPSFKVTG							: 179
cry8Aa	KVYDQKKAELIQCIGWAD-VMQSQSEEDLEGRND--ARTRSVSNSQDIAIDLNEVSSDQSFAVSG							: 190
cry10Aa	KNIIIVLTSITPTKQDQD-KYQEFFDKTPEPARTH--ANAKAHDLTTEPPIIDKPDMLKNNAS							: 194
cry16Aa	-----EVIGCMVIRTAIDQGKD-DYNNVUQKQDOP--KSTGNLSTWVTKTAEDSDENGAIHTVNNQGSP							: 193
cry19Ba	NDTLLRATSMSSHEMESN-IAHRAIAAKQK--NNFASGELLERSYIMDPEHLETRDHQSDFSLG							: 183
cry24Aa	-----ETDILGESESSNGVATYMDLGAEALNNKSN--INYQTQAEATKTEEREFTRQKGIVYRSS							: 182
	a g	y l w	f p					
	240	*	260	*	280	*	300	*
axmi007	-----TYKTLIIPFQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 284
crylAa	-----KQNPPLSIVVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 211
crylAc	-----KQNPPLSIVVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 211
crylIa	-----EENPLPITVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 239
cry3Aa1	-----EENPLPITVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 255
cry3Ba	-----EENPLPITVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 256
cry4Aa	PSDCDYHNLWVSSYQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 268
cry6Aa	-----MJDSSKTTLPRHS LIGHTIKLNSNKKC							: 51
cry7Aa	-----TENPLPITVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 238
cry8Aa	-----HAWLILIAVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 249
cry10Aa	-----QHPTPAWQAEIETUHMLKQFATYHNIULQ--QGINPSTFNSSNYQGYLKRKQIQEYDUCYI							: 260
cry16Aa	-----GHEVLLPISVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 254
cry19Ba	-----GHEVLLPISVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 243
cry24Aa	-----SNTTLLPITVQAAQAHFHLQOOGAELADEUNADIHPSQIEPNACTSDYK-LLKENIPKYSIMCANTY							: 239
	1 aqaen HI L da g	g	y	Y	Y	YC	Y	

Fig. 1A

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	*	320	*	340	*	360	*				
axm1007 :	REGGLMLKHEPNEPN	-----	MR-NS	I PAD	GYV	LTIVL	ITLQ	PSFMIDIKRKKDSIG--RIGGIKKEE	351		
crylAa :	NTIGERQMECPD	-----	SRD	WYR	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	272	
crylAc :	NTIGERQMECPD	-----	SRD	WYR	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	272	
crylAa :	STGLLMLKRCGTN	-----	AES	UWY	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	300	
cry3Aa1 :	NVGLDKKIRGCS	-----	YES	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	316	
cry3Ba :	NVGLMSRERST	-----	YDAN	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	317	
cry4Aa :	KKGLMLWQF	TPDSM	L	LDGNIN	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	335
cry6Aa :	QTGGLLPVNEQ	-----	OP	THVNL	S	PSF	MDFSQ	WVW	PSFMIDIKRKKDSIG--RIGGIKKEE	106	
cry7Aa :	NSGSGLRWN	EST	-----	YE	QWV	WVW	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	299
cry8Aa :	KIGGLDKKIRGT	-----	SKS	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	310	
cry10Aa :	WAGLTMIE	TMN	-----	AT	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	321
cry16Aa :	NKGGLMDFRTAG	-----	QW	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	313	
cry19Ba :	KSGGLESKQIIG	-----	LS	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	306	
cry24Aa :	TKGLMLWQF	EST	-----	AID	WVW	WQ	PRE	LTIVL	IVL	PSFMIDIKRKKDSIG--RIGGIKKEE	300
	GL	a	w	w	xx	v	5p	v	vp	1 466	

	380	*	400	*	420	*	440	*							
axmi007	:NF	FDRLTYLEIOPN	-----	:LAIMEYNLTSGIRLNSPDEP	:DIFYDJKNETYGNRLVGLIAMPNRSTYAH	-----	:TG	: 414							
cry1Aa	:LE	ENFDGSGFRG	-----	:MAORIEQMRDQ	:PHEDILSNSHTITD	:VVERHGFNYUSGHOITASPVGFSGCP	-----	:EF	: 333						
cry1Ac	:LE	ENFDGSGFRG	-----	:SAOGIERSH	:PHEDILSNSHTITD	:DAHRCYYYWUSGHOIMASPVGFSGCP	-----	:EF	: 333						
cry1Ia	:GT	VHPHPSTTIIWYNNNAPS	SAIEA	AVWEN	:PHEDILSNSHTITD	-----	:RWSJYMMUUCGH	-----	:KL	: 365					
cry3Aa1	:VG	VVNNLRYGV	-----	:TTFSNIENYERK	:PHEDILSNSHTITD	:FQFURFQP	-----	:GYVGNDSFNYU	:SCGNVYST	: 374					
cry3Ba	:FT	TLNALQEYQ	-----	:PTFSSIENSIER	:PHEDILSNSHTITD	:FQFURFQP	-----	:GYSGKD	:SFNYU	:SCGNVYET	: 375				
cry4Aa	:FE	ESPYKYYD	-----	:FQYQEDS	:PHEDILSNSHTITD	:SPNTBEKAOTT	:PPNNFTSHYNMFHYTLDNIS	-----	:Q	: 396					
cry6Aa	:KS	SANDIASY	-----	:FKVAGDPS	:PHEDILSNSHTITD	:SPNTBEKAOTT	:PPNNFTSHYNMFHYTLDNIS	-----	:Q	: 170					
cry7Aa	:SLS	ISNPNDIGP	-----	:SF	SUMENTALST	:PHEDILSNSHTITD	:YI	:TSKYKAF	:SHEI	:IQDPLFYUASAHKV	-----	:F	: 360		
cry8Aa	:AF	NISVTSTGFCNPWSTHSGI	LEYEVENN	WEP	:PHEDILSNSHTITD	:I	:TMSRGG	-----	:I	:TLMDAYINYU	:SGH	-----	:TL	: 377	
cry10Aa	:SDT	FRTITLELENG	-----	:L	TRN	:PHEDILSNSHTITD	:GFRY	:TNSRNS	-----	:D	:LDPYD	:IFSC	:GNCQMAF	: 374	
cry16Aa	:NG	EIYGLMTPYFS	-----	:FE	KAESLY	:PHEDILSNSHTITD	:KGFREVINSISY	:T	:FLSGG	:GONKYS	:TYNN	-----	:IN	: 376	
cry19Ba	:ND	HVVYGLMVPYIS	-----	:FE	HAESLY	:PHEDILSNSHTITD	:KGFREVINSIN	:SET	:FLSGG	:ENRY	:FLTHGE	-----	:IY	: 370	
cry24Aa	:GRT	DSPSGFDWINTG	-----	:RT	LANFND	:LE	:RE	:WTD	:SE	:V	:KQ	:GDMT	-----	:IY	: 373

	460	*	480	*	500	*	520	
axm1007	: TEI1YGERGTGPPTTKTLIIPFESYKVSVIVDROVPTSPFPNIYFTINQIELYLNNSPSNKLTYSGGNL							ENDKKT : 489
cry1Aa	: AFPLFGNAGNAAPP-VLVLSTLGLCIFRTRLSSPMLYRRIILGSGPNQNE-LFVLDGTEFSPASLTINLPSTIYRQ--							: 404
cry1Ac	: TFPFLYGTGMNAAPQQRIVAQLGQGVYRTLSTSDFPRPFN-IGINNQQ-LSVDLGTFAFG-TSSNLPSAVYRK--							: 403
cry1Ia	: EFRIT1GTLN1STQGSTNTSINPVTLPLFTSRDWRTESLAGLNLFLT-QPWNVGVRVD SHK KFVTHPIASDNFYV							: 439
cry3Aa1	: RPSIGSNDLITTSFPYGNKSEPVQNLEFMNGEK W RAVANTNLAVUPS-ASYSGVTKVEG S QYNDTDEASTUTYD							: 448
cry3Ba	: RPSIGSNDTITTSFPYGDKSIEPIKSLFDGQK W TAINTIADFAFPDGK1YVGTV W DSQYDDQKNETS T QTYD							: 450
cry4Aa	: KSSVYGMHNWTFDQLKSLGLATN1Y1FLNLNVISDNKYLNDYNN1SKMDFFITNGTR1LEKELTAGSGQ1YDVNK							: 471
cry6Aa	: QYEEAAKNIY1SDFLHGDQKLEGVINIOKRLKEVQTA1NQAHG-SSPAHKELLEVKVNKLTKLLE W IKAEQ							: 244
cry7Aa	: KKSEQNSNLYT1GIGKTCGIVSSGAYSFHGN W PTLIAAPSVV W Y-TQNYGVQE W YVGVKGHVHYRCDNKY-							: 433
cry8Aa	: KYRRTADSTVYTATYNGRITSEKNSFALEDRD W IEINSTVANLANY-QKAYGVPGCSUD W IVKRGTSSTIAYLYS							: 451
cry10Aa	: THTMDDRN1I1UJGAVHGN1I1SQDTSKVFFPYRNPKIDKVEIVRHR W ESD1Y1EM1FFSNSSEVFRYSSNS W IEENN-							: 448
cry16Aa	: EGSSFRGQD1TYDGGTSSTINIPYVYI1PUDG W PVNITKHNFSVTDNNSSKELIYGAHRTMKPVVR							: 451
cry19Ba	: NGCPFLGQDTEYVYI1D1SNNNS1Y1LNWLUTEMEY1WY W YPUGD W PVNITKHNFSVTDNNSSKELIYGAHRTMKPVVR							: 445
cry24Aa	: GRTD1VVMFRQDTAYEDPSTF1S11Y1DD1Y1LDR1AAAVST1QGAMDT1FGVSSSRP1D1RGRNQLYQSNKP-							: 447

Fig. 1B

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	* 620 *	* 640 *	* 660 *	
axmi007 :	KIITIMIPPAEGNSPDTSNKVIEEPCHTECMLVYLQSQG-----RLEETCRTPNSDQSYWTRVRYWAGAGNTL			: 626
cry1Aa :	SQMHQDPLT1STNMCGTSVVKCPCGTECDLHRTSPG-----QISTLRAVNITAPLSQYVWVNRVYASTTINLQPH			: 537
cry1Ac :	DSITQDPAVFGNFIIFNGSVIS-CPCGTGCDLVRINSSGGNNIQNRGYIEVPIHFPSTEYIWRVRYASVTPIHLN			: 542
cry11a :	WSITQDPLVKAFN1SSGAAWRCGFTGCDLHRTNTG-----TGFDIRVMINPPA0WVWVRYASTTDLQPH			: 574
cry3Aa1 :	KKTTQDPLVKAQK1QSGASWACCPPTGCDLHCTE-----NGSAATIYVTPDVSYSQKVRARHRYASTTQ1TET			: 584
cry3Ba :	EKTTQDPLVKAAYK1QSGASQIEGCGTGCMLFKESS---NSIAKFKVTLNSAALLQDWRVRYASTTINLRLF			: 589
cry4Aa :	HLTQDPAVANSCTASKVQOCRGHTGCDLHCDLFDK-----HFKETCQHSNFQDSYFURGTVASNSANTR			: 601
cry6Aa :	EAHKVFOKEOGIWIATIGAQHENLRTTISLQEVDQSDADEIQIELEDASDULVVAQEAEDFTLNAMNSRQNL			: 394
cry7Aa :	TKTQDPAVAKYKEDDPSTVKGCPGTECDLWKGSTG-----YIGDIKATVNSPLSOKWVWVRYAIVVSGQFN			: 564
cry8Aa :	DKTQDPAVIGDMDVYLGGSVVQCGCPTGCDLHRTNPS-----ILGTFAVTVNGSLSQYWRVRYASVTDFFET			: 593
cry10Aa :	DMTQDPAVAKLKESSDSKAVKCPGTECDLWVLLKDS-----MDFRVRFKLVWVROVWVRYAIVNAPKTV			: 574
cry16Aa :	DKTQDPAVVAASSINGSSISLKKCPGTECDLWVNRADS-----GLTMRFKALLLDKLVWVROVWVRYKCNSSKLI			: 577
cry19Ba :	DKTQDPAVTLNLEGANIKK-----GCHTGGDLRLEYR-----FLSLRIK-LIASTTRDTRVYASNSGQIM			: 568
cry24Aa :	DKTQDPAVAYERGRNSSWACCGTGCMLVNSYHS-----VWSFKVYCSELKWRWEDVYASHGNCQL			: 579

itq pa k gpgf3gg 6

q r r rya

	680	700	720	740	
axmi007 :	PNHSITLIPGVIGIPPPQLRNNMFGSGTNYN-----DQNGDGGFPPPSVTLPLNR--NIPFTFNRADYSN-SI1EDK				: 697
cry1Aa :	TSIDG-----RPINQCNFSA0MSSGS-----DQGSGSRTVYCHT1PPMFSNG-----SSVFTTSAHVFMSGNEWMDR				: 601
cry1Ac :	VNUGN-----SSTFSMTVPAATSLD-----DQSSDGGFESANAFTSSLG-----N-----TVGVRPFSGTAGV1MDR				: 603
cry11a :	TSIING-----KAINQGNFSADMNRGE-----DQDFTKRTYCHT1PFS1LDV-----QSTFTTGAUNFSSGNEWMDR				: 638
cry3Aa1 :	TSIDG-----APFNQYYFDK1LNKGD-----THTMNSNLASD1PPEFLSG-----NNLQ1GVTGLSAGDKWMDK				: 646
cry3Ba :	WQNSN-----MDFLVIYINK0MNDG-----DHTQDQEDATSNMNG1SCD-----TMDFIIGAESFVSNEK0WMDK				: 653
cry4Aa :	AVVNLISPG--VAELGMALNPFTSGTDYDQKQDQQLERSNEVKAQPNQ--NISLVFNRSEYVNTT1MDK				: 672
cry6Aa :	DNV1SDSCNCSTTNTMSNQYENP1TNTMSNQYVQYIISHEVTS1PNMFLSRN-----SNLEYKCPENNFM1YHYN				: 464
cry7Aa :	YV1ND-----K1TQTKFQNTVETT1EGKQD1TGSFEGV1EVS1T1Q1PDE-----HPK1T1LHS1L1SNSSFWDSH				: 631
cry8Aa :	LYEG-----DTEKNRFMK1MDNCA-----S1T1C1K1B1S1D1Q1RET-----QDK1L1SMG1FSSGQEWMDK				: 656
cry10Aa :	FLTG-----IDT1SVELPST1SRQNPNTAD1TAD1GCV1T1PRTVPMKTFEGEDT1L1TLYGTPNHSYD1MDK				: 644
cry16Aa :	FRWKCE-----GY1QQQIHN1SPTVG-----AFSYLES1T1T1E1N1D1T1M-----EV1PYGROFVEDIPS1I1EDK				: 642
cry19Ba :	UNMG-----YQNP1TYFN1LPT1TSRD-Y1ELKFED1QLVD1SY1MSGGP-----S1SNT1LWLDNFNSNGP1I1EDK				: 632
cry24Aa :	WKRUPS-----TGVAPRQUARHNVQGTFSNSDREAK1K1D1F1T1PEENN-----FAFT1LES1GGD1I1EDK				: 643

Y f

	760	780	800	
axmi007 :	EP1P1T1S1VRQNRE-----KOK1P1T1QTK1NTFF1NHT1KNT1LNIEATMYD1			: 744
cry1Aa :	EP1P1AEV1FEAEYD-----L1R1AK1A1E1E1T1SSNQ1IGL1K1D1V1D1Y1H1D1QVS			: 648
cry1Ac :	EP1P1V1A1LEA1EYD-----L1R1AK1A1E1E1T1ST1N1Q1L1K1N1V1D1Y1H1D1QVS			: 650
cry11a :	EP1P1EV1YEAEYD-----F1K1A1E1K1A1T1ST1N1P1R1L1K1D1V1D1Y1H1D1QVS			: 685
cry3Aa1 :	EP1P1P1-----			: 652
cry3Ba :	EP1P1P1-----			: 659
cry4Aa :	EP1P1T1S1RE1REDREK1Q1E1T1V1Q1D1T1F1P1A1P1K1N1L1Q1S1E1T1D1Y1D1Q1A1			: 722
cry6Aa :	DP1V1N1SD1W1Y1N-----			: 475
cry7Aa :	EP1P1D1V1Y1A1E1K1E-----L1E1A1K1A1T1E1E1-G1R1A1L1Q1D1V1D1Y1K1D1Q1S1			: 677
cry8Aa :	EP1P1D1E1Y1A1E1Q-----L1E1A1K1A1T1E1E1-G1R1C1A1L1T1K1D1-G1R1G1V1D1Y1V1Q1A1			: 702
cry10Aa :	EP1P1T1Q1V1L1D1Y1T1E1K1E1K1D1-----			: 675
cry16Aa :	EP1P1T1N-----			: 648
cry19Ba :	EP1P1G1L1LNQ1A1G-----Y1D1Y1D1Q1A1G-----			: 679
cry24Aa :	EP1P1V1G1SAFEYE1G1K1N1E1K1U1K1A1D1-----			: 674

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Fig. 1C

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